



Published in final edited form as:

Nat Hum Behav. 2022 November ; 6(11): 1577–1586. doi:10.1038/s41562-022-01408-5.

Rare genetic variants explain missing heritability in smoking

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Abstract

Common genetic variants explain less variation in complex phenotypes than inferred from family-based studies, and there is a debate on the source of this “missing heritability”. We investigated the contribution of rare genetic variants to tobacco use with whole-genome sequences from up to 26,257 unrelated individuals of European ancestries and 11,743 individuals of African ancestries. Across four smoking traits, SNP-based heritability (h^2_{SNP}) was estimated from .13 to .28 (SEs .10-.13) in European ancestries with 35–74% of it attributable to rare variants with minor allele frequencies between 0.01% and 1%. These heritability estimates are 1.5–4 times higher than past estimates based on common variants alone and accounted for 60% to 100% of our pedigree-based estimates of narrow-sense heritability (h^2_{ped} : .18-.34). In African ancestry samples, h^2_{SNP} was estimated from .03 to .33 (SEs .09-.14) across the four smoking traits. These results suggest that rare variants are important contributors to the heritability of smoking.

Keywords

Genetic architecture; tobacco; cigarettes; whole genome sequencing; addiction

Introduction

Characterizing genetic architecture of complex phenotypes is fundamental to understanding genetic influences on human individual differences and has implications in diverse fields including medicine and psychology. The joint distribution of genetic effect sizes and minor allele frequency (MAF) is shaped by natural selection and population history^{1,2} and informs our understanding of human evolution and gene-mapping strategies for complex traits. The past decade of genome-wide association studies (GWAS) of common genetic variants has expanded our knowledge of this genetic architecture by discovering tens of thousands of genomic loci associated with a wide range of complex phenotypes such as height³, lipids⁴, diabetes⁵, and schizophrenia⁶, to name a few. However, the aggregate

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Author contributions statement

SKJ, SV, MK, and LE designed the study. AF contributed to data analysis. All authors contributed to data collection and curation, and critically reviewed the manuscript.

Competing interests statement

Psaty serves on the Steering Committee of the Yale Open Data Access Project funded by Johnson & Johnson. EKS has received grant support from GSK and Bayer Research support to University of Pennsylvania from RenalytixAI and personal fees from Calico Labs, both outside the current work. The funders had no role in study design, data collection and analysis, decision to publish or preparation of the manuscript. Other authors declare no competing interests.

Code availability statement

All software used is publicly available and can be found at references cited.

effect of common genetic variation typically explains less phenotypic variation than that inferred from traditional family-based studies (e.g., twins, or siblings, or larger pedigrees)⁷, a difference often referred to as “missing heritability”.

Tobacco use is a complex behavioral trait of high public health concern^{8–10} and demonstrated genetic and environmental (e.g., policy) influences^{11,12}. Not only is tobacco use a leading cause of global morbidity and mortality, but measures of tobacco use are strong indicators of addiction to nicotine. For example, the number of cigarettes smoked per day is genetically highly correlated ($r=.95$) with nicotine dependence¹³ and other commonly used substances^{14,15}. Tobacco use is also considered a part of externalizing dimensions of personality and psychopathology along with other substance use and hyperactive behaviors¹⁶. Heritability of smoking behaviors has been estimated at approximately 50% (SE 5%)¹⁷ in twin studies, comparable to many other complex behavioral traits.

At the same time, estimates of tobacco use heritability from GWAS of single nucleotide polymorphisms (SNPs) have routinely found much lower SNP-based heritability (h^2_{SNP}) estimates^{18,19}. Such analyses to date have been based on common variants with MAF > 1% from GWAS of imputed microarrays. In a recent GWAS of tobacco use in up to 1.1 million individuals, Liu et al. reported h^2_{SNP} estimates ranging between 5% and 11%¹⁸ with smoking initiation and age of smoking initiation showing the highest and the lowest estimates, respectively¹⁸. Even more recently, Evans et al.²⁰ reported h^2_{SNP} estimates of 5%–18% for smoking traits in UK Biobank imputed genotypes of up to 323,068 individuals. In this latter study, the estimated contribution of rare variants to the heritability was minimal, likely due to poor imputation of rare variants <1% MAF. Similar to results for other complex traits^{17,21}, some but far from all of the twin-based heritability of smoking behaviors can be attributed to common variants obtained through imputation of microarray genotypes.

There is an extensive literature regarding the possible contributors to missing heritability, including inflated family-based heritability estimates²², increased phenotypic heterogeneity in GWAS compared to family-based studies²³, epistasis²⁴, and genetic variants not in linkage disequilibrium (LD) with common variants, including structural²¹ and rare variants²⁵. Rare genetic variants are one compelling explanation for the missing heritability of fitness-related traits, as one expects negative selection to force deleterious alleles to low frequencies^{26,27}. Common variants, on the other hand, are expected to explain most trait variance under a neutral model where most mutations have little selective effects^{27,28}. The contribution of rare variants can inform competing explanations for the missing heritability as well as competing population genetics models, but this requires large samples of extremely well-imputed microarrays or whole genome sequencing.

To date, SNP-based heritability estimates of complex behaviors have been based on a few million common variants. With imputed variants, the quality of imputation depends on the reference panel used^{29,30}, and even the best imputation strategies perform poorly for variants with MAF < 1% in population-based samples^{31,32} of unrelated individuals. With the advent of relatively affordable deep whole-genome sequencing (WGS), it is now possible to directly genotype variants of lower frequency in larger samples. While genetic association studies may be underpowered to detect an association between a given single rare variant

and a complex trait³³, recent extensions of mixed-effects models allows one to estimate a random effect representing the aggregate contribution of rare variants to phenotypic variance over and above common variation^{31,32}. To date, a small number of recent whole-genome sequencing studies have reported evidence that rare variants account for a substantial part of the heritability of anthropometric, transcriptomic, and medical phenotypes^{34–37} (but see also ^{38,39} for counterexamples). Notably, rare variants, especially those in regions of low LD, captured a large part of the missing heritability for height and BMI, albeit with large standard errors⁴⁰.

Here, we used deep whole-genome sequencing (mean depth 30x) from the Trans-Omics for Precision Medicine (TOPMed) program to estimate the heritability explained by variants as rare as MAF of 1 in 10,000 for individuals of European ancestry (up to 26,257 individuals), and 1 in 1,000 for African admixed individuals (up to 11,743 individuals). We performed extensive sensitivity analyses to test the influence of rare-variant population structure along with various analytic parameters on our SNP-based heritability estimates for tobacco use. The study protocol was approved by the Institutional Review Board at the University of Minnesota and the Trans-Omics for Precision Medicine (TOPMed) consortium. Informed consent was obtained originally by participating studies.

Results

Heritability estimates

We estimated heritability of four smoking phenotypes in samples of European ancestries: 1) age of smoking initiation (AgeSmk, N=14,709) which measures the age at which an individual started regularly smoking; 2) cigarettes smoked per day (CigDay, N=15,384), an index of heaviness of smoking and the average number of cigarettes smoked per day as a current or former smoker, grouped into five bins, with higher numbers indicating greater use; 3) smoking cessation (SmkCes, N =17,827), a binary variable indicating whether a person is a current smoker; and 4) smoking initiation (SmkInit, N=26,257), a binary variable indicating people who ever smoked regularly (i.e., over 100 cigarettes) in their life. We stratified SNPs and short indels by their MAF and linkage disequilibrium (LD) so that we have a total of six bins (MAF 5–50%-high LD, MAF 5–50%-low LD, MAF 1–5%-high LD, MAF 1–5%-low LD, MAF 0.1–1%, MAF 0.01–0.1%)³². Variants were assigned to the high-LD group when their LD scores were higher than the median of the variants in the same MAF bin (Table 1). After adjusting for the fixed effects of 10 common variant principle components (PCs), 10 rare variant PCs, age, sex, and a random effect of study, total SNP-based heritability (\hat{h}_{SNP}^2) from variants of all MAF was .226 (SE: .116) for AgeSmk, .134 (.095) for CigDay, .283 (.127) for SmkCes, and .225 (.096) for SmkInit (Fig. 1). Heritability estimates from the two common-variant bins (i.e., MAF 1–50%) – which includes one bin for variants with high LD scores and one bin for variants with low LD scores – were summed to compute total heritability attributable to common variants ($\hat{h}_{\text{common}}^2$). Rare-variant heritability (\hat{h}_{rare}^2) was computed likewise from the two MAF 0.01–1% bins, which were not grouped by LD score because most rare variants have low LD (see Methods). Across four smoking phenotypes, rare variants accounted for 35~74% of the total heritability. The majority of the heritability attributable to rare variants

was in the rarest frequency bin (MAF 0.01–0.1%), except for CigDay where most \hat{h}^2_{rare} was attributed to variants with MAF 0.1–1% (Supplementary Table 1). When we further partitioned rare variants into their functional impact, most of the heritability was localized to lower functional impact (non-protein altering) variants (Supplementary Table 2).

Sensitivity analyses

We used a variety of sensitivity analyses to evaluate the influence of residual population structure and cryptic relatedness.

First, we evaluated the influence of increasing the number of PCs from 20 to 40 and 100 (half of which derived from common and rare variants) on \hat{h}^2_{SNP} to test whether greater number of PCs account for potential residual population structure. Results for AgeSmk, SmkCes, and SmkInit were unaffected (Fig. 2 and Supplementary Table 3). We observed model convergence issues when correcting CigDay for large number of PCs, resulting in negative \hat{h}^2_{SNP} (e.g., -0.12) attributable to the rarest MAF bin, which we deemed well outside the plausible range.

Second, we tested whether \hat{h}^2_{SNP} , especially that of rare variants, were driven by individuals sharing long identity-by-descent (IBD) segments. Using FastSMC⁴¹, we detected about 7.5 million IBD segments longer than 2cM and shared among at least two individuals (mean length=2.50cM, SD=0.50cM). After removing up to 178 individuals whose shared IBD segments stretch longer than 2.5% of the total genome length, \hat{h}^2_{SNP} did not show meaningful differences with changes in \hat{h}^2_{SNP} ranging from -0.025 to 0.031 (Fig. 3 and Supplementary Table 3). Third, to assess the influence of distant family structure on heritability estimates, we adjusted for the top 20 PCs from an IBD-based relatedness matrix in addition to the 20 PCs from rare and common variants and found \hat{h}^2_{SNP} was not affected with the largest change in \hat{h}^2_{SNP} being 0.013 (Fig. 3 and Supplementary Table 3).

Fourth, previous studies indicated that rare variants are more likely to show geographical specificity⁴². While such geographic specificity was at least partially captured by our inclusion of study as a random effect, we went further by including a random effect of recruitment site (which is nested within a given study) in the model. After adjustment of site, \hat{h}^2_{rare} of SmkCes was about 50% of the original estimate while \hat{h}^2_{SNP} of other smoking traits showed little change (Fig. 3 and Supplementary Table 3).

Fifth, we obtained approximate null distribution of \hat{h}^2_{SNP} under the assumption that population structure explains the observed SNP-based heritability (i.e., genotypes of ancestrally close individuals are exchangeable). This was done by estimating \hat{h}^2_{SNP} in samples randomly permuted within individuals close in ancestry as determined by a weighted sum of top 10 PCs with weights proportional to their corresponding eigenvalues⁴³. We computed \hat{h}^2_{null} from 100 permuted trials and found limited evidence of inflation as

mean heritability estimates from permuted trials were near zero across all bins of four smoking phenotypes (Supplementary Table 4).

Sixth and finally, we estimated \hat{h}_{SNP}^2 in samples with decreasing control of population stratification by ascertaining samples with less stringent PC-based ancestry filtering thresholds (see Methods). The largest change in \hat{h}_{SNP}^2 was observed for SmkCes where the estimates were up to .10 higher in samples with less stringent PC-based filtering than in primary analysis, possibly reflecting sampling variations and residual population structure (Supplementary Fig.1 and Supplementary Table 3).

In summary, out of 36 comparisons (4 phenotypes \times 9 conditions), \hat{h}_{SNP}^2 showed relatively large changes ($\hat{h}_{SNP}^2 \pm .10$), only for SmkCes when we adjusted for geographical site, or relaxed ancestry filtering. Our primary results presented in Fig. 1 are from the most stringent PC-filtering condition.

Pedigree-based heritability estimates

We removed closely related individuals when estimating the heritabilities described above. However, we were able to leverage thousands of related family members in TOPMed to independently estimate total narrow-sense heritability of our four smoking phenotypes in pedigrees (\hat{h}_{ped}^2). These heritability estimates were derived using a single genetic relatedness matrix that included all individuals with at least one other close relative in TOPMed. The relatedness of closely related individuals was estimated from common variants which, when estimated for close family members, serves as a proxy for rare and common variant sharing. The relatedness of classically unrelated individuals (relatedness estimate ($\hat{\pi}$) $<.05$) was set to be zero (same as $K_{IBS>t}$ in Zaitlen et al, 2013²²). This procedure provides an upper bound on the narrow-sense heritability estimate, to which we can compare the estimates of \hat{h}_{SNP}^2 described in the previous section and quantify any of the remaining missing heritability.

Using related individuals in TOPMed across cohorts (N up to 21,546), narrow-sense heritabilities for AgeSmk, CigDay, SmkCes, and SmkInit were estimated .343 (.075), .175 (.066), .179 (.067) and .288 (.057), respectively. To check whether \hat{h}_{ped}^2 was downwardly estimated due to relatively large proportion of unrelated pairs, we also estimated pedigree-based heritability in Framingham Heart Study (N up to 3,024) which is composed of families as part of the study design. Similar estimates (AgeSmk .225, CigDay .244, SmkCes .195, SmkInit .299) were obtained in Framingham Heart Study as in the larger analysis of all available families, albeit with larger SEs. Estimates from pedigree analysis are presented in Fig. 3 and Supplementary Table 5.

Heritability estimates in African ancestries

We explored \hat{h}_{SNP}^2 attributable to variants with MAF down to 0.1–1% for SmkInit (N=11,743) and common variants for other smoking phenotypes (N=6,796–7,549). After

adjusting for 100 PCs, admixture proportions of five ancestries, local ancestry, and the same demographic covariates as in European ancestry, common-variant-based SNP heritability was estimated as following: .098 (.091) for AgeSmk, .028 (.113) for CigDay, .075 (.120) for SmkCes, and .085 (.10) for SmkInit. Variants from MAF 0.1–1% additionally accounted for about 24% of phenotypic variance of SmkInit, leading to total SNP-based heritability (combining both common and low frequency variants) of SmkInit: .329 (.144). Heritability estimates for individual bins are reported in Table 2 and Supplementary Table 6.

Discussion

Using up to 26,257 whole-genome sequences, we found that about 13–28% of phenotypic variance of four smoking phenotypes in European ancestry individuals could be attributed to genetic variants with minimum minor-allele frequencies as rare as 1 in 10,000. This is about 1.5–4.5 times larger than the previous SNP-based heritability estimates based on common variants alone.

This increase was largely driven by inclusion of rare variants with MAF 0.1–0.01%, which accounted for 35–74% of the estimated SNP-based heritability of smoking phenotypes in samples of European ancestries. Smoking cessation showed the highest \hat{h}_{rare}^2 (.209; SE .123), followed by age of smoking initiation (.153; SE .114), smoking initiation (.079; SE .091) and cigarettes per day (.054; SE .092). Different smoking phenotypes would in principle vary in their genetic architectures if they differentially relate to fitness or fitness-related traits. However, standard errors associated with these estimates prevent us from drawing strong conclusions about their relative magnitudes.

The contribution of rare variants observed here seem consistent with the action of negative selection. Under negative selection, harmful mutations are maintained at low frequency in the population, whereas under neutral model, common variants are expected to explain the majority (>90%) of the heritability²⁸. The same selective pressures may apply to the heritability patterns found for common variants in this study. We found that most of the heritability from common variants was attributed to low LD variants in European ancestry samples. Consistent with this, Gazal et al. 2017⁴⁴ reported that common variants with low LD in low-recombination rate regions had larger per-SNP heritability than those with high LD. One possible explanation for this finding is that low LD common variants are more likely to arise recently than high LD variants. Therefore, the low LD variants have had less time to be pushed to low frequency or fixation by selection pressure, comprising a major source of the heritability attributed to common variants⁴⁴.

Our suggestion that smoking traits have been under negative selection might seem surprising. While nicotine itself has been pervasive in the environment for millions of years, tobacco in its cigarette form represents an evolutionarily novel environment for humans and the selection against such traits is likely to be weak due to its recency. Nevertheless, genetic variants influencing smoking can affect multiple different traits more directly related to evolutionary fitness. For example, smoking is highly genetically correlated with age at onset of reproductive behaviors (especially with age of smoking initiation⁴⁵), and many social and health outcomes such as education and metabolic diseases. Therefore, selection pressure

on these correlated traits can influence genetic architecture of smoking phenotypes⁴⁵. More studies are needed to understand mechanisms that maintain the contribution of rare genetic variants to the heritability of smoking phenotypes in population.

We found that almost all the contribution from rare variants to \hat{h}^2_{SNP} was attributed to genetic variants classified as having relatively low expected protein altering consequences. This may suggest an importance of rare regulatory genetic variation in the etiology of smoking behaviors. Despite limited contributions to heritability from protein-altering variants, it is still possible that they explain higher heritability individually⁴⁰ given the smaller number of such variants (about 0.2 million protein-altering v.s. 20 million non-protein-altering variants in MAF 0.01–0.1%) and presumably higher selective pressure against them. Unfortunately, high standard errors and overall small heritabilities from protein altering variants bin prevented us from drawing strong conclusions in the present data.

Current SNP-based heritability estimates were largely robust to our sensitivity checks. Heritability changed little after increasing the number of PCs and testing finer-scale population structure via permutation. The estimates also largely remained unaffected by removing individuals that share several long IBD segments or adjusting for top 20 PCs from the IBD relatedness matrix. Controlling for site of recruitment led to about a 50% reduction in rare-variant heritability of smoking cessation, while the three other smoking phenotypes were little unaffected. One explanation is that genetic risk of smoking cessation is stratified geographically^{46,47} and rare variants are sensitive to capturing such ecological clustering. However, it is not clear why the same pattern is not observed for other closely related measures of smoking. Alternatively, for practical reasons, studies recruited samples from sites with systematic differences in current smoking rates or disease status (e.g., clinical samples versus community controls), leading to a site and smoking status confounded. Therefore, we consider \hat{h}^2_{SNP} of smoking cessation, obtained after adjusting for geographical site as a conservative lower bound.

There is a long, ongoing debate on the source of missing heritability for virtually all complex traits. We found that current \hat{h}^2_{SNP} accounted for 60% to 100% of the pedigree-based, narrow-sense heritability estimates (\hat{h}^2_{ped}) across the four phenotypes, closing the missing heritability gap for smoking phenotypes. Note that our \hat{h}^2_{ped} values are estimated from pedigrees from multiple cohorts, who also may span different generations (e.g., parents-offspring) and share markedly different smoking environments. We consider our \hat{h}^2_{ped} as the most relevant benchmark by which to compare \hat{h}^2_{SNP} from our GREML results and past GWAS studies which also have varying sources of sample heterogeneity, including gene-environment interaction⁴⁸ and varying heritability⁴⁹. Twin studies, on the other hand, usually consist of large homogeneous cohort with well-defined pedigrees sharing most of the demography (i.e., monozygotic and dizygotic twins).

For individuals of African ancestries, we found that common SNPs and indels (MAF > 1%) accounted for 3~15% of phenotypic variance of smoking phenotypes, similar in magnitude

to existing studies^{18,20}. We observed an additional contribution of rare variants (MAF 0.1–1%) for smoking initiation, accounting for about 25% of smoking initiation liability. Note that estimating heritability in samples with complex population structure is in its infancy and how recent admixture influences causal allele frequency spectrum is not well understood. More research on this topic will be welcome.

Our findings should be interpreted in light of several limitations. First, although we used the largest WGS sample reported to date for heritability analysis, even larger datasets will be important. Larger sample sizes would allow greater precision in estimation and a more comprehensive assessment of the genetic architecture of these complex traits by finer partitioning by MAF and functional annotations. Second, even with the use of deep sequences, we did not fully reach the trait heritability, either as estimated using available pedigrees, or twin heritability reported in the literature. There remain many explanations, including ultra-rare variants (MAF \leq .01%), other types of genetic variations (e.g., copy number variations) that are not in LD with the variants used here, and still other sources of heritable variation. Cigarettes per day showed the lowest SNP-based heritability and often encountered model convergence issues especially with a large number of covariates. Since it is a binned variable, its heritability may be more robustly estimated on liability scale⁵⁰.

Third, although we carefully assessed the potential influence of population structure in extensive sensitivity analyses, existing methods may not be entirely capturing population stratification of rare variants^{51,52}. More studies are needed to understand the extent and best ways to handle it, although we are also sensitive to the possibility that such corrections may be counterproductive, removing meaningful heritable variance.

Fourth, our pedigree-based heritability estimates may be inflated by shared environment as we were unable to model genetic similarity and environmental similarity separately. Therefore, pedigree estimates may best be interpreted as an upper-bound on the SNP-based narrow-sense heritability. However, we expect the magnitude of inflation due to shared environment to be smaller than in typical twin studies given that our pedigree sample includes multiple classes of family relations who share much less of their environments than twins would.

Fifth, there is ample documentation of spousal similarity in smoking behaviors^{53–55} and one of the potential sources of this similarity, assortative mating, can artifactually inflate marker-based heritability estimates⁵⁶. While recent studies have not found evidence for primary assortative mating on smoking traits in the genome⁵⁷, more research is needed on this topic.

Sixth, genetic association signals of human behavioral traits can arise from multiple sources, not only from variants' downstream biological influences on a phenotype of interest but also from its genetically correlated traits (e.g., education, income) along with indirect effect of parents and siblings' genetics^{58–60}. Current SNP-based heritability estimates include influences from multiple sources and could overlap with polygenic signals of socioeconomic factors given their substantial genetic correlations with smoking ($|r|=.26\sim.55$)¹⁸. With bigger sample sizes and studies of close families, future research can localize the origins of

SNP-based heritability and examine the genetic architecture of shared and distinct genetic components of smoking and its correlated phenotypes (e.g., education, income)⁶¹.

Seventh, smoking phenotypes were measured by one or two questions and were limited to those commonly collected in biomedical studies like those in TOPMed. This allows accumulations of large sample sizes across multiple independently-collected samples, but each measure is noisy and may reflect idiosyncrasies of participating studies. We attempted to account for the latter through inclusion of a random effect of study.

In conclusion, the present study expanded our understanding of the genetic architecture of tobacco use by showing that much of the missing heritability of smoking phenotypes can be explained by rare genetic variants. The use of WGS allows less biased estimation of SNP-based heritability by including virtually all potential causal SNPs down to a MAF of 0.01% in individuals of European ancestries and 0.1% in African ancestry, rather than relying on the degree to which imputed variants tag causal variants. The current study informs the genetic etiology of nicotine addiction and provides a benchmark for the future study of other complex behavioral traits.

Methods

Sample

We considered individuals of European ancestries in TOPMed (freeze 8, mean depth >30)⁶² measured for at least one of four smoking phenotypes for inclusion. Our data access application was approved by relevant cohorts in TOPMed. We determined European ancestries in two steps. First, we identified an initial ancestry-inclusive set by projecting TOPMed genotypes (N=137,977) onto genetic principal component (PC) axes from the 1000 Genomes project⁸ (1000G) then used a k-nearest neighbor method to assign ancestry of TOPMed individuals with 1000G as a reference set. More specifically, we used online augmentation-decomposition-transformation to calculate PC scores of TOPMed individuals, which implements Procrustes transformation with an augmented data set (i.e., combining TOPMed and 1000G reference genomes together; <https://github.com/daviddaiweizhang/fraposa>)⁶³. Then, for a given TOPMed sample, we chose the top 20 reference individuals in 1000G who were closest in terms of the Euclidean distance of 20 PC scores and assigned European ancestry when at least 87.5% of the reference individuals had European ancestry (Supplementary Note). This resulted in 38,915 individuals initially classified as European ancestry who also had at least one smoking phenotype. Second, after visually inspecting PCs 1–4 of the selected individuals, we suspected residual population heterogeneity, especially in PC 4 (Supplementary Fig. 2). We then further restricted samples to those whose summed Euclidean distance of PCs 1–4 fell within the 1 interquartile range (IQR) of the European sample (N=38,915) identified in the first step. We additionally created samples using 1.5, 2, 3 IQR and reserved them for sensitivity analysis (Supplementary Fig. 1–2). After IQR filtering, we only retained unrelated individuals. Relatedness was estimated with HapMap3 variants (HWE p -value > 10^{-6} , MAF > 0.01) using GCTAV1.92 to obtain a list of nominally unrelated individuals with pairwise relatedness ($\hat{\pi}$ < .025). We additionally removed 76–190 individuals who showed very high rare-variant sharing ($\hat{\pi}$ > .25 in MAF 0.01–0.1% bin) who seemed to have inherited small IBD segments inherited from distant non-European ancestors.

This resulted in the following final sample size per phenotype in Table 1 (N ranging from 14,709 to 26,257).

Phenotypes

TOPMed is a consortium of independent studies, where DNA samples were sequenced and called in a unified way. Smoking phenotypes had previously been collected independently in each of the constituent TOPMed studies. Four smoking phenotypes, each representing self-report questions assessing different stages of tobacco use, were available across most TOPMed studies. We used the same definition and coding scheme as Liu et al., 2019¹⁸. Age of smoking initiation (AgeSmk) measures the age at which an individual started regularly smoking. Cigarettes smoked per day (CigDay) was the average number of cigarettes smoked per day as a current or former smoker and grouped into five bins with higher numbers indicating greater use. For both AgeSmk and CigDay, lifelong non-smokers are excluded (set to missing). Smoking cessation (SmkCes) and initiation (SmkInit) are binary variables indicating former versus current smokers and never versus ever regular smoker, with case defined as current and ever smoker, respectively. These four variables were correlated but not redundant, each measuring distinct aspects of smoking (Supplementary Note, Supplementary Table 7). Descriptive statistics for each phenotype across cohorts can be found in Supplementary Table 8.

Genotypes, LD scores, GRM, and GREML-LDMS-I

Genome-based restricted maximum likelihood (GREML) estimates heritability by comparing phenotypic similarity to observed genetic similarity among distantly related individuals using a linear mixed model⁶⁴. GREML yields biased estimates when causal variants are unevenly distributed as a function of LD and MAF³¹. To mitigate this bias, the GREML-LDMS-I method partitions SNPs into different LD \times MAF bins³². We initially considered ~710 million genotypes that passed strict quality filters described elsewhere⁶⁵. We additionally removed 95,750 variants with Hardy-Weinberg equilibrium p -values less than 10^{-6} in the European ancestry sample (N=38,915). Then, we calculated allele frequency separately for each phenotype using `plink1.9` in a final sample that went through PC, IQR, and relatedness filtering. We stratified variants by MAF and then further stratified by linkage disequilibrium (LD) scores using the median LD scores within the two most common MAF bins. This resulted in six bins: MAF (0.05, 0.5] high LD, MAF (0.05, 0.5] low LD, MAF (0.01, 0.05] high LD, MAF (0.01, 0.05] low LD, MAF (0.001, 0.01], and finally MAF (0.0001, 0.001]. We stratified only the common variant bins by LD because most low-frequency and rare variants have low LD scores, and because more bins decrease estimate precision. LD scores, defined as the sum of squared correlations (r^2) between a variant and all the variants in a region, were calculated using `GCTA1.92` with default 10Mb window in the final sample combined across four smoking phenotypes (summary of LD scores presented in Supplementary Table 9). This process resulted in approximately 35 million SNPs and indels (Table 1).

For each phenotype, we performed GREML-LDMS-I with the GRMs for the above-mentioned six bins and cohort indicator matrix as random effects. The cohort matrix was an $N \times N$ matrix indicating whether a given pair of individuals belongs to the

same study (1, otherwise 0). The variance explained by cohort was included in total phenotypic variance, which could yield somewhat smaller heritability estimates than when the heritability is conditioned on cohort. We regressed out age, age², sex and their two-way interaction terms^{66–68} from quantitative phenotypes (i.e., AgeSmk and CigDay) and used residuals. Residuals of CigDay were further inverse-rank normalized to facilitate model convergence by smoothing its distribution. GREML-LDMS-I results from other types of transformations for AgeSmk and CigDay are presented in Supplementary Table 3. We calculated 10 PCs from common variants (MAF \geq 1%) and another 10 PCs from rare variants (0.01% $<$ MAF $<$ 1%) after LD pruning (plink –indep-pairwise 100 5 0.2 for common and 2000 10 0.02 for rare variants). These 20 PCs and sequencing center were entered as fixed effects in linear mixed model. The same demographic variables and 20 PCs were entered as fixed effects for binary variables. We used GCTAV1.92 for both construction of GRM and GREML-LDMS-I analysis. We replaced original GRM diagonals with 1+ inbreeding coefficients (Fhat3 computed from the GCTA software) given the original formula tended to yield far higher variance of diagonals for rare variants than expected in theory (Supplementary Table 10)⁶⁹. We allowed the estimates to be negative to obtain unbiased estimates. Heritabilities for binary phenotypes were analyzed under a liability threshold model⁷⁰. Population prevalence was set at 0.15 and 0.42 for SmkCes and SmkInit, respectively, based on smoking prevalence in the UK Biobank dataset, to allow for ready comparison with this publicly available and widely-used dataset. For all traits, total heritability was calculated by adding heritability estimates of the six bins with SEs approximated by the delta method⁷¹.

Partitioning rare variant heritability

To further interrogate sources of rare-variant heritability, we divided rare variant bins into protein-altering versus non-protein-altering variant bins⁷². Functional impact of variants was assessed by snpEff 4.3 with “HIGH” and “MODERATE” impact categorized as protein-altering while “LOW” and “MODIFIER” categorized as non-protein-altering⁷³. “HIGH” includes variants expected to have a disruptive impact in the protein, such as protein truncation and loss of function. “MODERATE” includes variants that are expected to influence effectiveness of the protein, such as missense and splice region variants. “MODIFIER” and “LOW” includes variants that influences non-coding genes or located in non-coding region and are usually considered harmless to protein behaviors. Details of this classification can be found in its website (https://pcingola.github.io/SnpEff/se_inputoutput/). Variance components were then estimated for a total of eight bins.

Sensitivity analyses

To evaluate the degree of sensitivity of our results to residual population structure, especially that of rare variants, and various analytic decisions, we conducted extensive sensitivity analyses. First, we performed GREML-LDMS-I with 40 PCs (20 common, 20 rare) and 100 PCs (50 common, 50 rare) as fixed effects. Second, we estimated heritability after removing individuals whose total length of shared IBD segments stretch more than 2.5% of the genome (N=121–177 depending on phenotypes) to test whether heritability attributed to rare variants is primarily driven by a subset of samples sharing recent ancestors and presumably higher environmental similarity. Third, we also adjusted for 20 PCs from the IBD-based

relatedness matrix, in addition to the 10 PCs from common variants and 10 PCs from rare variants (40 total PCs). IBD-segments were estimated using 632,008 common variants (LD pruned by plink --indep-pairwise 1,000 50 0.6) with FastSMC⁷⁰ with default settings, except we set the minimum IBD length $\geq 2\text{cM}$. We used decoding files precomputed by the authors of FastSMC and only retained IBD segments with quality score > 0.1 . The IBD-based GRM matrix was created by summing the length of the shared IBD segments in a given pair of individuals and dividing it by the length of the diploid human genome ($3608 \times 2 \text{cM}$). Then, we derived principal components from the IBD-based relatedness matrix. Fourth, we added 53 recruitment sites nested within the cohorts as random effects. This additional control is meant to better account for rare variants that may geographically cluster. Fifth, we performed GREML-LDMS-I with permuted samples within genetically close neighbors^{35,43,74}. For this, we created an $N \times N$ distance matrix populated by scaled Euclidian distance of PC 1–10 calculated from LD-pruned common variants for every pair of individuals. Then, we randomly exchanged genotypes of a given individual with one of their 100 nearest neighbors using sampling algorithms from LocPerm which is developed to control for populations structure in rare variant association test⁴³. We estimated heritability in 100 replicates of permuted genotypes with the same demographic covariates and cohort used in the main analysis. Mean (\hat{h}_{null}^2) and SD of heritability estimates from 100 replicates were calculated for each bin and were tested against zero using a one-sided Z-test as heritability is bounded above zero (Supplementary Note). Last, we estimated heritability in samples with increasingly less strict PC-based ancestry filtering mentioned earlier (1.5, 2, 3 IQR). The greater the IQR threshold, the more ancestral variation can be present in the resulting sample, the larger the sample, and the greater the chance of observing effects of population stratification.

Pedigree-based heritability

We created a GRM with all available samples including related ones after excluding pairs related greater than .80 to exclude identical twins and duplicates. To aid in model identification, we included cohorts that had at least 10 first-degree relatives defined as relatedness greater than .375. A list of cohorts included in this analysis is presented in Supplementary Table 11. We created GRM using common variants (MAF $> 5\%$) and set GRM entries of pairs related less than .05 as zero and retained the rest of the entries as they were. This GRM was fitted together with a cohort matrix and the same set of fixed effect covariates used in the primary analysis. To test whether resulting \hat{h}_{ped}^2 is underestimated due to relatively low level of relatedness structure in the sample, we repeated the analysis without a random effect of cohort, using only Framingham Heart Study (FHS) which has high proportions of related individuals.

SNP-based heritability in African ancestries

We initially had 19,788 individuals who had either one of smoking phenotypes and were classified as African ancestry by the ancestry assignment procedure described earlier. We selected unrelated individuals ($\hat{\pi} < 0.025$) by applying `pcairPartition` function in the GENESIS package on kinship coefficients from `pcrelate`⁷⁵ where familial relatedness is estimated with MAF ($< 1\%$) and LD-pruned ($|\text{LD}| < .32$) variants after accounting for

population structure. We additionally excluded 58 individuals who showed more than two-way admixture as determined by global ancestry proportions of either South-Central Asia, East Asia, Native America, or Middle East greater than 10%. This resulted in sample size in Table 2. The resulting samples were predominantly African ancestry with recent European ancestry admixture (mean African ancestry proportion=83% (SD: 8.9%) and mean European ancestry proportion=15% (SD: 8.4%)). Ancestry proportions of each individual were estimated from local ancestry inference by RFMix⁷⁶ which estimates ancestry of admixed individuals at each genomic segment of two homologous chromosomes, using the Human Genome Diversity Panel (HGDP) as a reference panel⁷⁷ (Supplementary Fig. 3). Given the smaller sample size of African ancestry samples, we restricted the variants to be analyzed to MAF 0.1–1% for SmkInit (N=11,744) and common variants for the other three phenotypes (N=6,796~7,549). We applied the same analytic procedure as in European ancestry samples: 1) selected genetic variants with MAF > 2 and HWE *p*-value > 10⁻⁶, 2) partitioned variants into MAF (0.05, 0.5] high LD, MAF (0.05, 0.5] low LD, MAF (0.01, 0.05] high LD, MAF (0.01, 0.05] low LD, and additionally MAF (0.001, 0.01] for SmkInit (Table 2), 3) calculated GRM for each bin and performed GREML-LDMS-I with the same set of demographic and cohort covariates as in European ancestry analyses. We additionally included 50 common- and 50 rare variant-based PCs, global ancestry proportions of five continents (Sub-Saharan Africa, South-Central Asia, East Asia, Native America, and Middle East) as fixed effects and local ancestry kinship (Supplementary Note) as a random effect to account for complex population structure in the admixed sample^{43,44}. Pedigree heritability was not estimated for individuals of African ancestries as SNP-based relatedness is no longer proportional to IBD in admixed population⁷⁸.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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Acknowledgements

Molecular data for the Trans-Omics in Precision Medicine (TOPMed) program was supported by the National Heart, Lung and Blood Institute (NHLBI). See the TOPMed Omics Support Table (Supplementary Note) for study specific omics support information. Core support including centralized genomic read mapping and genotype calling, along with variant quality metrics and filtering were provided by the TOPMed Informatics Research Center (3R01HL-117626-02S1; contract HHSN268201800002I). Core support including phenotype harmonization, data management, sample-identity QC, and general program coordination were provided by the TOPMed Data Coordinating Center (R01HL-120393; U01HL-120393; contract HHSN268201800001I). We gratefully acknowledge the studies and participants who provided biological samples and data for TOPMed.

Funding:

R01DA044283, R01DA037904, R01HG008983 to SIV

R01MH100141 to MCK

Cohort-wise acknowledgement in Supplementary Note

Data availability statement

Phenotypes are available through authorized access portal in dbgap (<https://dbgap.ncbi.nlm.nih.gov/>) or direct request to TOPMed Principal Investigators. Accession numbers and email addresses of Principal Investigator are presented in Supplementary Note. Genetic data are available through dbgap TOPMed exchange area.

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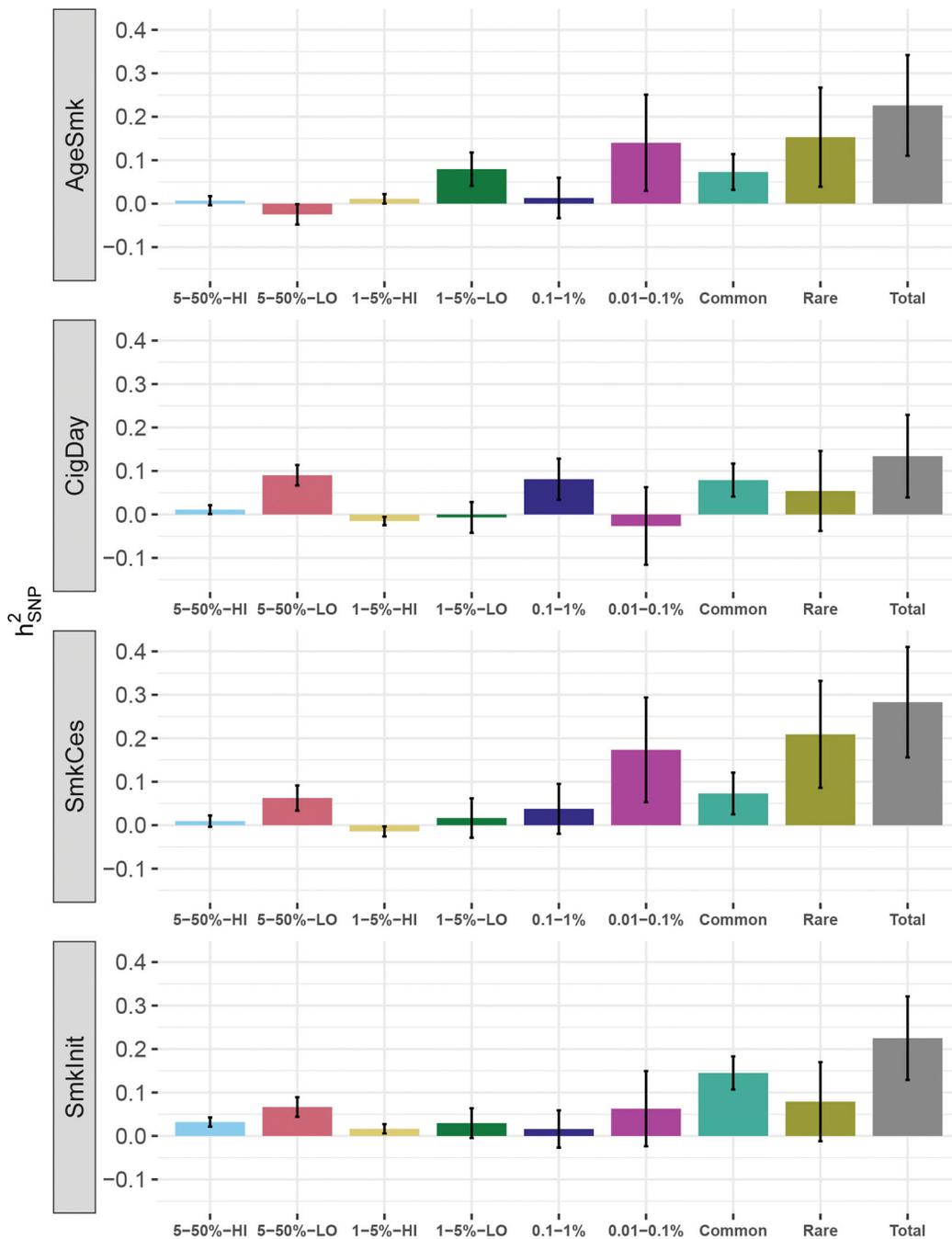


Figure 1. SNP-based heritability estimates in the European ancestry sample for each of the six MAF/LD bins, and sums across bins. Error bars represent standard errors. The “Rare” bin is the sum of the MAF 0.1–1% and MAF 0.01–0.1%. “Common” is the sum of the other MAF bins. “Total” is the sum of “Rare” and “Common”. HI and LO each indicate high and low LD. All estimates were adjusted for by demographic variables and 20 PCs (half of them from rare variants) as fixed effects along

with random effect of cohort except for CigDay which was adjusted for 5 common PCs to allow model convergence.

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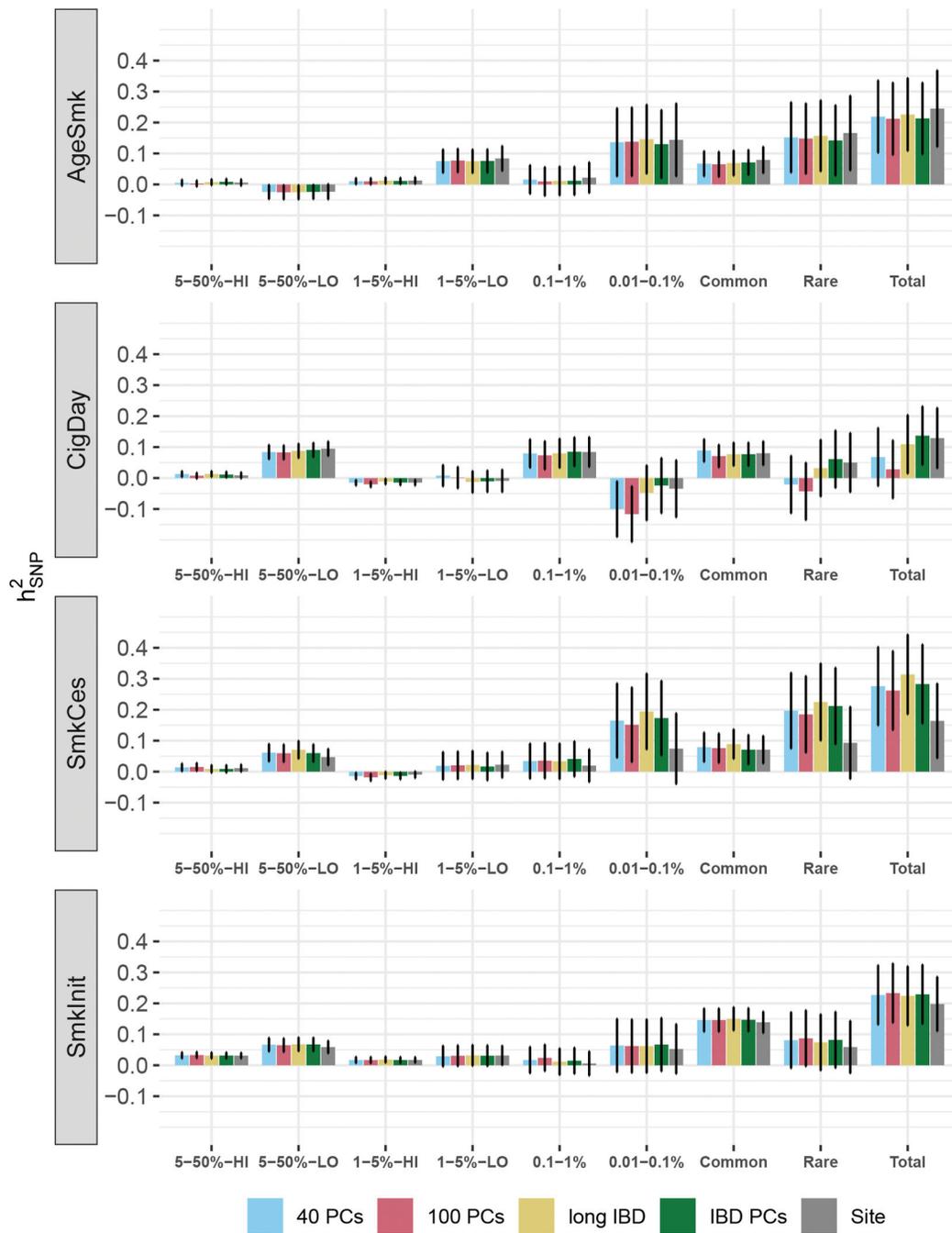


Figure 2. SNP-based heritability estimates in the European ancestry sample from sensitivity analyses. Error bars represent standard errors. The figure shows SNP-based heritability estimates from different sensitivity conditions. Heritability was estimated after adjusting for 20 common and 20 rare variant PCs (“40 PCs”), 50 common and 50 rare variant PCs (“100 PCs”), after removing individuals who share IBD segments more than 2.5% of the total genome length (“long IBD”), after adjusting for the top 20 PCs from the IBD-based GRM matrix (“IBD PCs”), and after adjusting for recruitment site as a random effect (“Site”).

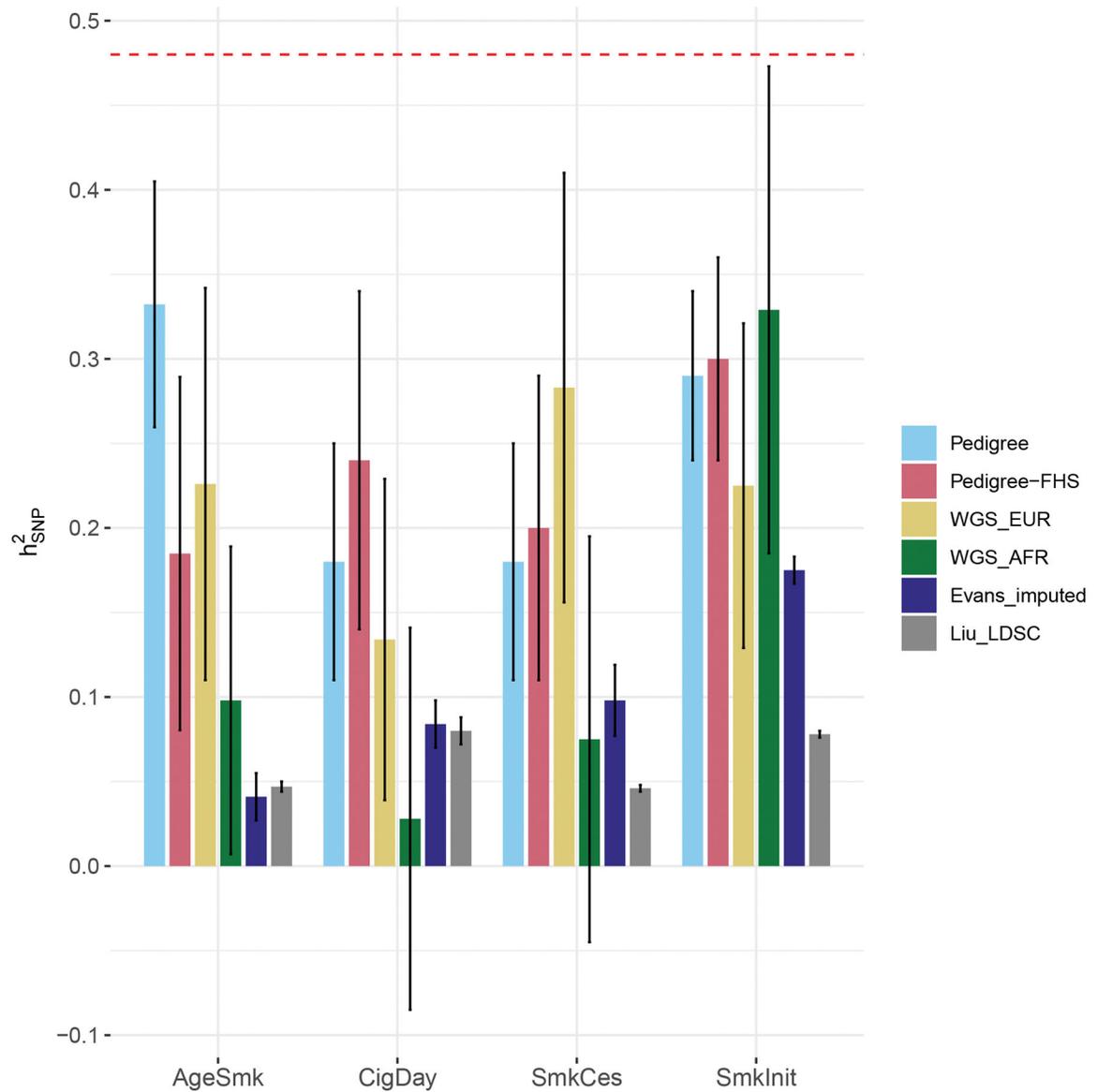


Figure 3.

Comparison of heritability estimates between current and published studies.

The figure shows SNP heritability estimates across different studies. Error bars denote standard errors. “Pedigree” and “Pedigree-FHS” refer to \hat{h}_{ped}^2 from whole TOPMed pedigree samples and FHS only. “WGS_EUR” and “WGS_AFR” refer to WGS-based SNP heritability estimates in individuals of European and African ancestries. Note that WGS_AFR is based on common variants only for all phenotypes except for SmkInit which includes the contribution from MAF 0.1–1% variants additionally. “Evans_imputed” and “Liu_LDSC” each refer to SNP heritability estimates from Evans et al. (MAF:1–50%, relatedness threshold=.02⁷⁹) and LDSC analysis from a recent meta-analysis of tobacco use¹⁸. The red dotted line indicates the heritability estimate of smoking from a recent large meta-analysis of twin studies¹⁷.

Table 1.

Sample size and number of variants per MAF/LD bin in European ancestry sample

	Number of variants per bin (MAF and Linkage Disequilibrium) ^a						
	Sample size ^b	5–50% - HI ^c	5–50% - LO	1–5% - HI	1–5% - LO	0.1–1%	0.01–0.1%
AgeSmk	14,709	3,092,517	3,092,534	1,342,734	1,342,736	5,392,813	28,280,118
CigDay	15,384	3,092,240	3,092,269	1,341,881	1,341,882	5,435,505	20,415,037
SmkCes	17,827	3,092,593	3,092,594	1,340,764	1,340,771	5,413,019	23,483,166
SmkInit	26,257	3,092,454	3,092,475	1,341,068	1,341,071	5,395,579	21,108,704

^aThis shows the number of variants per bin in IIQR unrelated samples ($\hat{\pi} < .025$).^bSample size of unrelated individuals^cHI=high LD, LO=low LD

Table 2.

Number of variants and SNP-based heritability in African Ancestry sample

	Number of SNPs					Sample size
	5–50% -HI	5–50% -LO	1–5% - HI	1–5% - LO	0.1–1%	
AgeSmk	4,298,268	4,298,322	3,415,787	3,415,847	-	6,909
CigDay	4,298,370	4,298,421	3,412,719	3,412,799	-	6,796
SmkCes	4,296,858	4,296,926	3,416,336	3,416,395	-	7,549
SmkInit	4,297,927	4,297,954	3,411,149	3,411,191	13,667,521	11,743

	\hat{h}_{SNP}^2					Total ^a
	5–50% -HI	5–50% -LO	1–5% - HI	1–5% - LO	0.1–1%	
AgeSmk	.089 (.043)	-.028 (.082)	.016 (.051)	.022 (.099)		.098 (.091)
CigDay	.076 (.041)	.001 (.084)	-.013 (.048)	-.036 (.109)	-	.028 (.113)
SmkCes	.008 (.040)	.060 (.090)	.031 (.054)	-.024 (.115)	-	.075 (.120)
SmkInit	.052 (.035)	.023 (.072)	-.022 (.041)	.031 (.095)	.243 (.133)	.329 (.144)

^aTotal=sum across five bins with MAF 0.1–50% for SmkInit and sum across four bins with MAF1–50% for the rest